

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Vinkemeier, Uwe
Darnell, Jr., James E.
- (ii) TITLE OF INVENTION: PURIFIED STAT PROTEINS AND METHODS OF
PURIFYING THEREOF
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patent In Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-182 N
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Human Stat91
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Gln	Trp	Tyr	Glu	Leu	Gln	Gln	Leu	Asp	Ser	Lys	Phe	Leu	Glu	15
1				5					10							
Gln	Val	His	Gln	Leu	Tyr	Asp	Asp	Ser	Phe	Pro	Met	Glu	Ile	Arg	Gln	30
				20				25								
Tyr	Leu	Ala	Gln	Trp	Leu	Glu	Lys	Gln	Asp	Trp	Glu	His	Ala	Ala	Asn	45
				35				40								
Asp	Val	Ser	Phe	Ala	Thr	Ile	Arg	Phe	His	Asp	Leu	Leu	Ser	Gln	Leu	60
				50			55					60				

Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
 65 70 75 80
 His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
 85 90 95
 Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
 100 105 110
 Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
 115 120 125
 Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
 130 135 140
 Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
 145 150 155 160
 Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
 165 170 175
 Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
 180 185 190
 Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
 195 200 205
 Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
 210 215 220
 Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
 225 230 235 240
 Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
 245 250 255
 Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
 260 265 270
 Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
 275 280 285
 Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
 290 295 300
 Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
 305 310 315 320
 Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser

420	425	430
Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu 435 440 445		
Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu 450 455 460		
Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu 465 470 475 480		
Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala 485 490 495		
Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg 500 505 510		
Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly 515 520 525		
Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys 530 535 540		
Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser 545 550 555 560		
Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly 565 570 575		
Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys 580 585 590		
Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg 595 600 605		
Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly 610 615 620		
Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser 625 630 635 640		
Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala 645 650 655		
Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp 660 665 670		
Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro 675 680 685		
Glu Pro Met Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr 690 695 700		
Glu Leu Ile Ser Val Ser Glu Val His Pro Ser Arg Leu Gln Thr Thr 705 710 715 720		
Asp Asn Leu Leu Pro Met Ser Pro Glu Glu Phe Asp Glu Val Ser Arg 725 730 735		
Ile Val Gly Ser Val Glu Phe Asp Ser Met Met Asn Thr Val 740 745 750		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ser Gln Trp Tyr Glu Leu Gln Gln Leu Asp Ser Lys Phe Leu Glu
 1           5           10           15
Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln
          20           25           30
Tyr Leu Ala Gln Trp Leu Glu Lys Gln Asp Trp Glu His Ala Ala Asn
          35           40           45
Asp Val Ser Phe Ala Thr Ile Arg Phe His Asp Leu Leu Ser Gln Leu
          50           55           60
Asp Asp Gln Tyr Ser Arg Phe Ser Leu Glu Asn Asn Phe Leu Leu Gln
          65           70           75           80
His Asn Ile Arg Lys Ser Lys Arg Asn Leu Gln Asp Asn Phe Gln Glu
          85           90           95
Asp Pro Ile Gln Met Ser Met Ile Ile Tyr Ser Cys Leu Lys Glu Glu
          100          105          110
Arg Lys Ile Leu Glu Asn Ala Gln Arg Phe Asn Gln Ala Gln Ser Gly
          115          120          125
Asn Ile Gln Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser
          130          135          140
Lys Val Arg Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile
          145          150          155          160
Lys Ser Leu Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr
          165          170          175
Leu Gln Asn Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln
          180          185          190
Lys Gln Glu Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn
          195          200          205
Lys Arg Lys Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr
          210          215          220
Glu Leu Thr Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys
          225          230          235          240
Arg Arg Gln Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu
          245          250          255
Asp Gln Leu Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln
          260          265          270
Val Arg Gln Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr
          275          280          285
Tyr Glu His Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg
          290          295          300
Thr Phe Ser Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu
          305          310          315          320

```

Arg Gln Pro Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys
 325 330 335
 Thr Gly Val Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln
 340 345 350
 Glu Leu Asn Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val
 355 360 365
 Asn Glu Arg Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly
 370 375 380
 Thr His Thr Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu
 385 390 395 400
 Ala Ala Glu Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly
 405 410 415
 Thr Arg Thr Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser
 420 425 430
 Leu Ser Phe Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu
 435 440 445
 Glu Thr Thr Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu
 450 455 460
 Pro Ser Gly Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu
 465 470 475 480
 Pro Arg Asn Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala
 485 490 495
 Gln Leu Ser Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg
 500 505 510
 Gly Leu Asn Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly
 515 520 525
 Pro Asn Ala Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys
 530 535 540
 Glu Asn Ile Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser
 545 550 555 560
 Ile Leu Glu Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly
 565 570 575
 Cys Ile Met Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys
 580 585 590
 Asp Gln Gln Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg
 595 600 605
 Glu Gly Ala Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly
 610 615 620
 Glu Pro Asp Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser
 625 630 635 640
 Ala Val Thr Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala
 645 650 655
 Glu Asn Ile Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp
 660 665 670
 Lys Asp His Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro

675					680					685					
Glu	Pro	Met	Glu	Leu	Asp	Gly	Pro	Lys	Gly	Thr	Gly	Tyr	Ile	Lys	Thr
690					695					700					
Glu	Leu	Ile	Ser	Val	Ser	Glu	Val								
705					710										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 582 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Thr Val Met Leu Asp Lys Gln Lys Glu Leu Asp Ser Lys Val Arg
 1 5 10 15
 Asn Val Lys Asp Lys Val Met Cys Ile Glu His Glu Ile Lys Ser Leu
 20 25 30
 Glu Asp Leu Gln Asp Glu Tyr Asp Phe Lys Cys Lys Thr Leu Gln Asn
 35 40 45
 Arg Glu His Glu Thr Asn Gly Val Ala Lys Ser Asp Gln Lys Gln Glu
 50 55 60
 Gln Leu Leu Leu Lys Lys Met Tyr Leu Met Leu Asp Asn Lys Arg Lys
 65 70 75 80
 Glu Val Val His Lys Ile Ile Glu Leu Leu Asn Val Thr Glu Leu Thr
 85 90 95
 Gln Asn Ala Leu Ile Asn Asp Glu Leu Val Glu Trp Lys Arg Arg Gln
 100 105 110
 Gln Ser Ala Cys Ile Gly Gly Pro Pro Asn Ala Cys Leu Asp Gln Leu
 115 120 125
 Gln Asn Trp Phe Thr Ile Val Ala Glu Ser Leu Gln Gln Val Arg Gln
 130 135 140
 Gln Leu Lys Lys Leu Glu Glu Leu Glu Gln Lys Tyr Thr Tyr Glu His
 145 150 155 160
 Asp Pro Ile Thr Lys Asn Lys Gln Val Leu Trp Asp Arg Thr Phe Ser
 165 170 175
 Leu Phe Gln Gln Leu Ile Gln Ser Ser Phe Val Val Glu Arg Gln Pro
 180 185 190
 Cys Met Pro Thr His Pro Gln Arg Pro Leu Val Leu Lys Thr Gly Val
 195 200 205

Gln Phe Thr Val Lys Leu Arg Leu Leu Val Lys Leu Gln Glu Leu Asn
 210 215 220
 Tyr Asn Leu Lys Val Lys Val Leu Phe Asp Lys Asp Val Asn Glu Arg
 225 230 235 240
 Asn Thr Val Lys Gly Phe Arg Lys Phe Asn Ile Leu Gly Thr His Thr
 245 250 255
 Lys Val Met Asn Met Glu Glu Ser Thr Asn Gly Ser Leu Ala Ala Glu
 260 265 270
 Phe Arg His Leu Gln Leu Lys Glu Gln Lys Asn Ala Gly Thr Arg Thr
 275 280 285
 Asn Glu Gly Pro Leu Ile Val Thr Glu Glu Leu His Ser Leu Ser Phe
 290 295 300
 Glu Thr Gln Leu Cys Gln Pro Gly Leu Val Ile Asp Leu Glu Thr Thr
 305 310 315 320
 Ser Leu Pro Val Val Val Ile Ser Asn Val Ser Gln Leu Pro Ser Gly
 325 330 335
 Trp Ala Ser Ile Leu Trp Tyr Asn Met Leu Val Ala Glu Pro Arg Asn
 340 345 350
 Leu Ser Phe Phe Leu Thr Pro Pro Cys Ala Arg Trp Ala Gln Leu Ser
 355 360 365
 Glu Val Leu Ser Trp Gln Phe Ser Ser Val Thr Lys Arg Gly Leu Asn
 370 375 380
 Val Asp Gln Leu Asn Met Leu Gly Glu Lys Leu Leu Gly Pro Asn Ala
 385 390 395 400
 Ser Pro Asp Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys Glu Asn Ile
 405 410 415
 Asn Asp Lys Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser Ile Leu Glu
 420 425 430
 Leu Ile Lys Lys His Leu Leu Pro Leu Trp Asn Asp Gly Cys Ile Met
 435 440 445
 Gly Phe Ile Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys Asp Gln Gln
 450 455 460
 Pro Gly Thr Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg Glu Gly Ala
 465 470 475 480
 Ile Thr Phe Thr Trp Val Glu Arg Ser Gln Asn Gly Gly Glu Pro Asp
 485 490 495
 Phe His Ala Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser Ala Val Thr
 500 505 510
 Phe Pro Asp Ile Ile Arg Asn Tyr Lys Val Met Ala Ala Glu Asn Ile
 515 520 525
 Pro Glu Asn Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp Lys Asp His
 530 535 540
 Ala Phe Gly Lys Tyr Tyr Ser Arg Pro Lys Glu Ala Pro Glu Pro Met
 545 550 555 560
 Glu Leu Asp Gly Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTCTCAGT GGTACGAACT TCAGCAGCTT GACTCAAAAT TCCTGGAGCA GGTTCACCAG	60
CTTTATGATG ACAGTTTTCC CATGGAAATC AGACAGTACC TGGCACAGTG GTTAGAAAAG	120
CAAGACTGGG AGCAGCTGC CAATGATGTT TCATTTGCCA CCATCCGTTT TCATGACCTC	180
CTGTACAGC TGGATGATCA ATATAGTCGC TTTCTTTGG AGAATAACTT CTTGCTACAG	240
CATAACATAA GGAAAAGCAA GCGTAATCTT CAGGATAATT TTCAGGAAGA CCCAATCCAG	300
ATGTCTATGA TCATTTACAG CTGTCTGAAG GAAGAAAGGA AAATTCTGGA AAACGCCAG	360
AGATTTAATC AGGCTCAGTC GGGGAATATT CAG	393

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAATTCCA TATGAGCACA GTGATGTTAG ACAAAC

36

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGATCCTAT TAGTGAACCT CAGACACAGA AATC

34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCACAGTGA TGTTAGACAA ACAGAAAGAG CTTGACAGTA AAGTCAGAAA TGTGAAGGAC	60
AAGGTTATGT GTATAGAGCA TGAAATCAAG AGCCTGGAAG ATTTACAAGA TGAATATGAC	120
TTCAAATGCA AAACCTTGCA GAACAGAGAA CACGAGACCA ATGGTGTGGC AAAGAGTGAT	180
CAGAAACAAG AACAGCTGTT ACTCAAGAAG ATGTATTTAA TGCTTGACAA TAAGAGAAAAG	240
GAAGTAGTTC AAAAAATAAT AGAGTTGCTG AATGTCACTG AACTTACCCA GAATGCCCTG	300
ATTAATGATG AACTAGTGGA GTGGAAGCGG AGACAGCAGA GCGCCTGTAT TGGGGGGCCG	360
CCCAATGCTT GCTTGGATCA GCTGCAGAAC TGGTTCAC TA GTTGCGGA GAGTCTGCAG	420
CAAGTTCGGC AGCAGCTTAA AAAGTTGGAG GAATTGGAAC AGAAATACAC CTACGAACAT	480
GACCCTATCA CAAAAACAA ACAAGTGTTA TGGGACCGCA CCTTCAGTCT TTTCCAGCAG	540
CTCATTCAGA GCTCGTTTGT GGTGGAAGA CAGCCCTGCA TGQCAACGCA CCCTCAGAGG	600
CCGCTGGTCT TGAAGACAGG GGTCCAGTTC ACTGTGAAGT TGAGACTGTT GGTGAAATTG	660
CAAGAGCTGA ATTATAATTT GAAAGTCAAA GTCTTATTTG ATAAAGATGT GAATGAGAGA	720
AATACAGTAA AAGGATTTAG GAAGTTCAAC ATTTTGGGCA CGCACACAAA AGTGATGAAC	780
ATGGAGGAGT CCACCAATGG CAGTCTGGCG GCTGAATTC GGCACCTGCA ATTGAAAGAA	840
CAGAAAAATG CTGGCACCAG AACGAATGAG GGTCTCTCA TCGTTACTGA AGAGCTTCAC	900
TCCCTTAGTT TTGAAACCCA ATTGTGCCAG CCTGGTTTGG TAATTGACCT CGAGACGACC	960
TCTCTGCCCC TTGTGGTGAT CTCCAACGTC AGCCAGCTCC CGAGCGGTTG GGCCTCCATC	1020
CTTTGGTACA ACATGCTGGT GGCGGAACCC AGGAATCTGT CCTTCTTCCT GACTCCACCA	1080
TGTGCACGAT GGGCTCAGCT TTCAGAAGTG CTGAGTTGGC AGTTTTCTTC TGTACCAAAA	1140
AGAGGTCTCA ATGTGGACCA GCTGAACATG TTGGGAGAGA AGCTTCTTGG TCCTAACGCC	1200
AGCCCCGATG GTCTCATTCC GTGGACGAGG TTTTGTAAGG AAAATATAAA TGATAAAAAT	1260
TTTCCCTTCT GGCTTTGGAT TGAAAGCATC CTAGAACTCA TTAAAAACA CCTGCTCCCT	1320
CTCTGGAATG ATGGGTGCAT CATGGGCTTC ATCAGCAAGG AGCGAGAGCG TGCCCTGTTG	1380
AAGGACCAGC AGCCGGGGAC CTTCTGCTG CGGTTCACTG AGAGCTCCCG GGAAGGGGCC	1440
ATCACATTCA CATGGGTGGA GCGGTCCAG AACGGAGGCG AACCTGACTT CCATGCGGTT	1500
GAACCCTACA CGAAGAAAGA ACTTTCTGCT GTTACTTTCC CTGACATCAT TCGCAATTAC	1560
AAAGTCATGG CTGCTGAGAA TATTCCTGAG AATCCCCTGA AGTATCTGTA TCCAAATATT	1620
GACAAAGACC ATGCCTTTGG AAAGTATTAC TCCAGGCCAA AGGAAGCACC AGAGCCAATG	1680
GAACTTGATG GCCCTAAAGG AACTGGATAT ATCAAGACTG AGTTGATTTT TGTGTCTGAA	1740
GTTCAC	1746

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid